

SEQUENCE LISTING

<110> Liang, Yanbin
Woodward, David F.

<120> Human Prostaglandin DP Receptor Variants
and Methods of Using Same

<130> 66872-029 (AR5747)

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1171

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (888)

<400> 1

atg aag tcg ccg ttc tac cgc tgc cag aac acc acc tct gtg gaa aaa	48
Met Lys Ser Pro Phe Tyr Arg Cys Gln Asn Thr Thr Ser Val Glu Lys	
1 5 10 15	

ggc aac tcg gcg gtg atg ggc ggg gtg ctc ttc agc acc ggc ctc ctg	96
Gly Asn Ser Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu	
20 25 30	

ggc aac ctg ctg gcc ctg ggg ctg ctg gcg cgc tcg ggg ctg ggg tgg	144
Gly Asn Leu Leu Ala Leu Gly Leu Leu Ala Arg Ser Gly Leu Gly Trp	
35 40 45	

tgc tcg cgg cgt cca ctg cgc ccg ctg ccc tcg gtc ttc tac atg ctg	192
Cys Ser Arg Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu	
50 55 60	

gtg tgt ggc ctg acg gtc acc gac ttg ctg ggc aag tgc ctc cta agc	240
Val Cys Gly Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser	
65 70 75 80	

ccg gtg gtg ctg gct gcc tac gct cag aac ccg agt ctg ccg gtg ctt	288
Pro Val Val Leu Ala Ala Tyr Ala Gln Asn Arg Ser Leu Arg Val Leu	
85 90 95	

gcg ccc gca ttg gac aac tcg ttg tgc caa gcc ttc gcc ttc ttc atg	336
Ala Pro Ala Leu Asp Asn Ser Leu Cys Gln Ala Phe Ala Phe Phe Met	
100 105 110	

tcc ttc ttt ggg ctc tcc tcg aca ctg caa ctc ctg gcc atg gca ctg Ser Phe Phe Gly Leu Ser Ser Thr Leu Gln Leu Leu Ala Met Ala Leu 115 120 125	384
gag tgc tgg ctc tcc cta ggg cac cct ttc ttc tac cga cgg cac atc Glu Cys Trp Leu Ser Leu Gly His Pro Phe Phe Tyr Arg Arg His Ile 130 135 140	432
acc ctg cgc ctg ggc gca ctg gtg gcc ccg gtg gtg agc gcc ttc tcc Thr Leu Arg Leu Gly Ala Leu Val Ala Pro Val Val Ser Ala Phe Ser 145 150 155 160	480
ctg gct ttc tgc gcg cta cct ttc atg ggc ttc ggg aag ttc gtg cag Leu Ala Phe Cys Ala Leu Pro Phe Met Gly Phe Gly Lys Phe Val Gln 165 170 175	528
tac tgc ccc ggc acc tgg tgc ttt atc cag atg gtc cac gag gag ggc Tyr Cys Pro Gly Thr Trp Cys Phe Ile Gln Met Val His Glu Glu Gly 180 185 190	576
tcg ctg tcg gtg ctg ggg tac tct gtg ctc tac tcc agc ctc atg gcg Ser Leu Ser Val Leu Gly Tyr Ser Val Leu Tyr Ser Ser Leu Met Ala 195 200 205	624
ctg ctg gtc ctc gcc acc gtg ctg tgc aac ctc ggc gcc atg cgc aac Leu Leu Val Leu Ala Thr Val Leu Cys Asn Leu Gly Ala Met Arg Asn 210 215 220	672
ctc tat gcg atg cac cgg cgg ctg cag cgg cac ccg cgc tcc tgc acc Leu Tyr Ala Met His Arg Arg Leu Gln Arg His Pro Arg Ser Cys Thr 225 230 235 240	720
agg gac tgt gcc gag ccg cgc gcg gac ggg agg gaa gcg tcc cct cag Arg Asp Cys Ala Glu Pro Arg Ala Asp Gly Arg Glu Ala Ser Pro Gln 245 250 255	768
ccc ctg gag gag ctg gat cac ctc ctg ctg ctg gcg ctg atg acc gtg Pro Leu Glu Glu Leu Asp His Leu Leu Leu Leu Ala Leu Met Thr Val 260 265 270	816
ctc ttc act atg tgt tct ctg ccc gta att gca ttt gtt cct gga gtc Leu Phe Thr Met Cys Ser Leu Pro Val Ile Ala Phe Val Pro Gly Val 275 280 285	864
ccc gcc aag aca cct ggg agt agg tgaggcttga ggaaacattt tcagtgtctgc Pro Ala Lys Thr Pro Gly Ser Arg 290 295	918
tcctctcctt tctcccaagt atcgcgctta ctatggagca tttaaggatg tcaaggagaa aaacaggacc tctgaagaag cagaagacct ccgagccttg cgatttctat ctgtgatttc aattgtggac ccttgattt ttatcatttt cagatctcca gtatttcgga tattttttca caagattttc attagacctc ttaggtacag gagccggtgc agcaattcca ctaacatgga 978 1038 1098 1158	

atccagtcctg tga

1171

<210> 2

<211> 296

<212> PRT

<213> Homo sapiens

<400> 2

Met	Lys	Ser	Pro	Phe	Tyr	Arg	Cys	Gln	Asn	Thr	Thr	Ser	Val	Glu	Lys
1				5				10					15		
Gly	Asn	Ser	Ala	Val	Met	Gly	Gly	Val	Leu	Phe	Ser	Thr	Gly	Leu	Leu
			20					25					30		
Gly	Asn	Leu	Leu	Ala	Leu	Gly	Leu	Leu	Ala	Arg	Ser	Gly	Leu	Gly	Trp
		35					40					45			
Cys	Ser	Arg	Arg	Pro	Leu	Arg	Pro	Leu	Pro	Ser	Val	Phe	Tyr	Met	Leu
	50					55				60					
Val	Cys	Gly	Leu	Thr	Val	Thr	Asp	Leu	Leu	Gly	Lys	Cys	Leu	Leu	Ser
65				70						75				80	
Pro	Val	Val	Leu	Ala	Ala	Tyr	Ala	Gln	Asn	Arg	Ser	Leu	Arg	Val	Leu
				85				90						95	
Ala	Pro	Ala	Leu	Asp	Asn	Ser	Leu	Cys	Gln	Ala	Phe	Ala	Phe	Phe	Met
			100					105				110			
Ser	Phe	Phe	Gly	Leu	Ser	Ser	Thr	Leu	Gln	Leu	Leu	Ala	Met	Ala	Leu
		115					120					125			
Glu	Cys	Trp	Leu	Ser	Leu	Gly	His	Pro	Phe	Phe	Tyr	Arg	Arg	His	Ile
	130					135					140				
Thr	Leu	Arg	Leu	Gly	Ala	Leu	Val	Ala	Pro	Val	Val	Ser	Ala	Phe	Ser
145					150					155					160
Leu	Ala	Phe	Cys	Ala	Leu	Pro	Phe	Met	Gly	Phe	Gly	Lys	Phe	Val	Gln
			165					170						175	
Tyr	Cys	Pro	Gly	Thr	Trp	Cys	Phe	Ile	Gln	Met	Val	His	Glu	Glu	Gly
		180					185						190		
Ser	Leu	Ser	Val	Leu	Gly	Tyr	Ser	Val	Leu	Tyr	Ser	Ser	Leu	Met	Ala
	195					200					205				
Leu	Leu	Val	Leu	Ala	Thr	Val	Leu	Cys	Asn	Leu	Gly	Ala	Met	Arg	Asn
	210					215					220				
Leu	Tyr	Ala	Met	His	Arg	Arg	Leu	Gln	Arg	His	Pro	Arg	Ser	Cys	Thr
225				230					235					240	
Arg	Asp	Cys	Ala	Glu	Pro	Arg	Ala	Asp	Gly	Arg	Glu	Ala	Ser	Pro	Gln
			245					250					255		
Pro	Leu	Glu	Glu	Leu	Asp	His	Leu	Leu	Leu	Leu	Ala	Leu	Met	Thr	Val
		260					265						270		
Leu	Phe	Thr	Met	Cys	Ser	Leu	Pro	Val	Ile	Ala	Phe	Val	Pro	Gly	Val
	275						280					285			
Pro	Ala	Lys	Thr	Pro	Gly	Ser	Arg								
	290					295									

<210> 3

<211> 1080

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1080)

<400> 3

atg aag tcg ccg ttc tac cgc tgc cag aac acc acc tct gtg gaa aaa	48
Met Lys Ser Pro Phe Tyr Arg Cys Gln Asn Thr Thr Ser Val Glu Lys	
1 5 10 15	
ggc aac tcg gcg gtg atg ggc ggg gtg ctc ttc agc acc ggc ctc ctg	96
Gly Asn Ser Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu	
20 25 30	
ggc aac ctg ctg gcc ctg ggg ctg ctg gcg cgc tcg ggg ctg ggg tgg	144
Gly Asn Leu Leu Ala Leu Gly Leu Leu Ala Arg Ser Gly Leu Gly Trp	
35 40 45	
tgc tcg cgg cgt cca ctg cgc ccg ctg ccc tcg gtc ttc tac atg ctg	192
Cys Ser Arg Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu	
50 55 60	
gtg tgt ggc ctg acg gtc acc gac ttg ctg ggc aag tgc ctc cta agc	240
Val Cys Gly Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser	
65 70 75 80	
ccg gtg gtg ctg gct gcc tac gct cag aac cgg agt ctg cgg gtg ctt	288
Pro Val Val Leu Ala Ala Tyr Ala Gln Asn Arg Ser Leu Arg Val Leu	
85 90 95	
gcg ccc gca ttg gac aac tcg ttg tgc caa gcc ttc gcc ttc ttc atg	336
Ala Pro Ala Leu Asp Asn Ser Leu Cys Gln Ala Phe Ala Phe Phe Met	
100 105 110	
tcc ttc ttt ggg ctc tcc tcg aca ctg caa ctc ctg gcc atg gca ctg	384
Ser Phe Phe Gly Leu Ser Ser Thr Leu Gln Leu Leu Ala Met Ala Leu	
115 120 125	
gag tgc tgg ctc tcc cta ggg cac cct ttc ttc tac cga cgg cac atc	432
Glu Cys Trp Leu Ser Leu Gly His Pro Phe Phe Tyr Arg Arg His Ile	
130 135 140	
acc ctg cgc ctg ggc gca ctg gtg gcc ccg gtg gtg agc gcc ttc tcc	480
Thr Leu Arg Leu Gly Ala Leu Val Ala Pro Val Val Ser Ala Phe Ser	
145 150 155 160	
ctg gct ttc tgc gcg cta cct ttc atg ggc ttc ggg aag ttc gtg cag	528
Leu Ala Phe Cys Ala Leu Pro Phe Met Gly Phe Gly Lys Phe Val Gln	
165 170 175	
tac tgc ccc ggc acc tgg tgc ttt atc cag atg gtc cac gag gag ggc	576
Tyr Cys Pro Gly Thr Trp Cys Phe Ile Gln Met Val His Glu Glu Gly	
180 185 190	
tcg ctg tcg gtg ctg ggg tac tct gtg ctc tac tcc agc ctc atg gcg	624

Ser	Leu	Ser	Val	Leu	Gly	Tyr	Ser	Val	Leu	Tyr	Ser	Ser	Leu	Met	Ala	
	195						200					205				
ctg	ctg	gtc	ctc	gcc	acc	gtg	ctg	tgc	aac	ctc	ggc	gcc	atg	cgc	aac	672
Leu	Leu	Val	Leu	Ala	Thr	Val	Leu	Cys	Asn	Leu	Gly	Ala	Met	Arg	Asn	
	210						215				220					
ctc	tat	gcg	atg	cac	cgg	cgg	ctg	cag	cgg	cac	ccg	cgc	tcc	tgc	acc	720
Leu	Tyr	Ala	Met	His	Arg	Arg	Leu	Gln	Arg	His	Pro	Arg	Ser	Cys	Thr	
225					230					235					240	
agg	gac	tgt	gcc	gag	ccg	cgc	gcg	gac	ggg	agg	gaa	gcg	tcc	cct	cag	768
Arg	Asp	Cys	Ala	Glu	Pro	Arg	Ala	Asp	Gly	Arg	Glu	Ala	Ser	Pro	Gln	
			245						250					255		
ccc	ctg	gag	gag	ctg	gat	cac	ctc	ctg	ctg	ctg	gcg	ctg	atg	acc	gtg	816
Pro	Leu	Glu	Glu	Leu	Asp	His	Leu	Leu	Leu	Leu	Ala	Leu	Met	Thr	Val	
			260					265					270			
ctc	ttc	act	atg	tgt	tct	ctg	ccc	gta	att	tat	cgc	gct	tac	tat	gga	864
Leu	Phe	Thr	Met	Cys	Ser	Leu	Pro	Val	Ile	Tyr	Arg	Ala	Tyr	Tyr	Gly	
	275						280					285				
gca	ttt	aag	gat	gtc	aag	gag	aaa	aac	agg	acc	tct	gaa	gaa	gca	gaa	912
Ala	Phe	Lys	Asp	Val	Lys	Glu	Lys	Asn	Arg	Thr	Ser	Glu	Glu	Ala	Glu	
	290					295					300					
gac	ctc	cga	gcc	ttg	cga	ttt	cta	tct	gtg	att	tca	att	gtg	gac	cct	960
Asp	Leu	Arg	Ala	Leu	Arg	Phe	Leu	Ser	Val	Ile	Ser	Ile	Val	Asp	Pro	
305					310					315					320	
tgg	att	ttt	atc	att	ttc	aga	tct	cca	gta	ttt	cgg	ata	ttt	ttt	cac	1008
Trp	Ile	Phe	Ile	Ile	Phe	Arg	Ser	Pro	Val	Phe	Arg	Ile	Phe	Phe	His	
				325					330					335		
aag	att	ttc	att	aga	cct	ctt	agg	tac	agg	agc	cgg	tgc	agc	aat	tcc	1056
Lys	Ile	Phe	Ile	Arg	Pro	Leu	Arg	Tyr	Arg	Ser	Arg	Cys	Ser	Asn	Ser	
			340					345				350				
act	aac	atg	gaa	tcc	agt	ctg	tga									1080
Thr	Asn	Met	Glu	Ser	Ser	Leu	*									
		355														

<210> 4
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Lys Ser Pro Phe Tyr Arg Cys Gln Asn Thr Thr Ser Val Glu Lys
 1 5 10 15
 Gly Asn Ser Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu

	20		25		30
Gly	Asn	Leu	Leu	Ala	Leu
	35		40		45
Cys	Ser	Arg	Arg	Pro	Leu
	50		55		60
Val	Cys	Gly	Leu	Thr	Val
	65		70		75
Pro	Val	Val	Leu	Ala	Ala
			85		90
Ala	Pro	Ala	Leu	Asp	Asn
			100		105
Ser	Phe	Phe	Gly	Leu	Ser
			115		120
Glu	Cys	Trp	Leu	Ser	Leu
			130		135
Thr	Leu	Arg	Leu	Gly	Ala
			145		150
Leu	Ala	Phe	Cys	Ala	Leu
			165		170
Tyr	Cys	Pro	Gly	Thr	Trp
			180		185
Ser	Leu	Ser	Val	Leu	Gly
			195		200
Leu	Leu	Val	Leu	Ala	Thr
			210		215
Leu	Tyr	Ala	Met	His	Arg
			225		230
Arg	Asp	Cys	Ala	Glu	Pro
			245		250
Pro	Leu	Glu	Glu	Leu	Asp
			260		265
Leu	Phe	Thr	Met	Cys	Ser
			275		280
Ala	Phe	Lys	Asp	Val	Lys
			290		295
Asp	Leu	Arg	Ala	Leu	Arg
			305		310
Trp	Ile	Phe	Ile	Ile	Phe
			325		330
Lys	Ile	Phe	Ile	Arg	Pro
			340		345
Thr	Asn	Met	Glu	Ser	Ser
			355		

<210> 5

<211> 10

<212> PRT

<213> Homo sapiens

<400> 5

Leu Pro Val Ile Ala Phe Val Pro Gly Val

1

5

10

<210> 6
<211> 14
<212> PRT
<213> Homo sapiens

<400> 6
Ala Phe Val Pro Gly Val Pro Ala Lys Thr Pro Gly Ser Arg
1 5 10

<210> 7
<211> 12
<212> DNA
<213> Homo sapiens

<400> 7
cgtaattgca tt 12

<210> 8
<211> 16
<212> DNA
<213> Homo sapiens

<400> 8
tcccgttaatt gcattg 16

<210> 9
<211> 12
<212> DNA
<213> Homo sapiens

<400> 9
ccaagtatcg cg 12

<210> 10
<211> 16
<212> DNA
<213> Homo sapiens

<400> 10
tcccgaagtat cgcgcg 16

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
tgatgaccgt gctcttcact 20

<210> 12

<211> 20
<212> DNA
<213> Homo sapiens

<400> 12
gatagaaatc gcaaggctcg